

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2000, 18:35:10 : Search time 23795.2 Seconds
(without alignments)
967.486 Million cell updates/sec

Title: US-09-227-881-34
Perfect score: 5271
Sequence: 1 attctgttcagttaccctc.....tcgggcacatgagccagcaag 5271

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_pac:*
6: gb_ph:*
7: gb_pl1:*
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92: gb_sts2:*
93: gb_v11:*
94: gb_v12:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5271	100.0	5300	11 AF007562	AF007562 Homo sapi
2	5233.4	98.3	79376	65 HS454G6	298750 Human DNA
3	5181.4	98.3	170425	77 AC024490	AC024490 Homo sapi
4	1804.4	34.2	2800	66 HSMTOC1	AF045791 Homo sapi
5	394.4	7.5	1086	66 HSGCL1A1	297171 Homo sapien
6	394.4	7.5	1228	9 AB0068651	AB006865 Homo sapi
7	189.8	3.6	161577	10 AC007688	AC007688 Homo sapi
8	189.8	3.6	193123	71 AC023790	AC023790 Homo sapi
9	189	3.6	199722	77 AC012404	AC012404 Homo sapi
10	187.8	3.6	97037	9 AC004973	AC004973 Homo sapi
11	187.8	3.6	135038	67 HUMWXXD703	L78810 Homo sapien
12	185.8	3.5	76727	65 HS821D11	AL021453 Human DNA

C	13	185.8	3.5	157044	79	AC026395	Homo sapi
C	14	185.8	3.5	157057	78	AC025997	Homo sapi
C	15	185.8	3.5	161499	72	AC015488	Homo sapi
C	16	185.8	3.5	184656	86	AL161726	Homo sapi
C	17	185.8	3.5	200681	69	AC008755	Homo sapi
C	18	185.6	3.5	201372	86	AL157941	Homo sapi
C	19	184.8	3.5	165190	89	AP001813	Homo sapi
C	20	184.8	3.5	163494	89	AP002391	Homo sapi
C	21	184.8	3.5	183241	89	AP001354	Homo sapi
C	22	184.6	3.5	176029	11	AC011362	Homo sapi
C	23	184.2	3.5	130020	67	HUAC004525	Homo sapi
C	24	184	3.5	157304	78	AC024720	Homo sapi
C	25	184	3.5	187709	73	AC016168	Homo sapi
C	26	184	3.5	233734	70	AC011407	Homo sapi
C	27	183.6	3.5	62070	88	AL138852	Homo sapi
C	28	183.6	3.5	129370	88	AP000505	Homo sapi
C	29	183.6	3.5	169333	89	AP002789	Homo sapi
C	30	183.6	3.5	193171	71	AC018723	Homo sapi
C	31	183.4	3.5	414071	11	AC053467	Homo sapi
C	32	183.4	3.5	149138	78	AC026936	Homo sapi
C	33	183.4	3.5	156331	90	HSJ193M1	Homo sapi
C	34	183.4	3.5	174974	87	AL136055	Homo sapi
C	35	183.4	3.5	195364	85	HS431A14	Human DNA S
C	36	183.4	3.5	198583	74	AC019114	AC019114 Homo sapi
C	37	183.2	3.5	41936	33	CH19R30879	AD000684 Homo sapi
C	38	183.2	3.5	70128	10	AC007536	AC007536 Homo sapi
C	39	183.2	3.5	119483	9	AC005588	AC005588 Homo sapi
C	40	183.2	3.5	145528	9	AC003665	AC003665 Homo sapi
C	41	183.2	3.5	167943	65	HS267M20	AL031053 Human DNA
C	42	183.2	3.5	170345	65	HS109F14	AL023271 Human DNA
C	43	183	3.5	42886	69	AC000093	AC000093 Homo sapi
C	44	183	3.5	91748	10	AC007748	AC007748 Homo sapi
C	45	183	3.5	112748	10	AC007242	AC007242 Homo sapi

ALIGNMENTS

Query Match	100.0%	Score 5271:	DB 11:	Length 5300:
Best Local Similarity	100.0%	Pred. No. 0:		
Matches 5271: Conservative	0:	Mismatches	0:	Indels
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				0
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1 ANCTTTGTTCACTTATACCTCAGGCGCATATATGAATGAATGATGAATACCAATATGTAAG 60				
Qy 61 tccataaactgtataagcctccatccgtgaatgtatgtcttcttgccaggaatgataaagaatca 120				
61 TCCCTATAAAGCTTATATAGCCCTCATTCGGATGTATGCTTTGGCAGGATATATAAGATCA 120				
Qy 121 ggaagaagagatcccaagcttagccaagtgccaggctgtgtcgtgtcttaatttagtga 180				
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Qy 181 cgaatgttgctccctgacagaagctatctcttcaggaaacatcacatccaaatagtgaaatc 240				
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RESULT	1
LOCUS	AF007562
DEFINITION	AF007562 5300 bp DNA
ACCESSION	AF007562
VERSION	AF007562.1
KEYWORDS	GI:2970123
SOURCE	human.
ORGANISM	.Homo sapiens
REFERENCE	Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.
AUTHORS	Nguyen,T.D., Chen,P., Huang,W.D., Chen,H., Johnson,D. and Polansky,J.R.
TITLE	Gene structure and properties of TIGR, an olfactomedin-related glycoprotein cloned from glucocorticoid-induced trabecular meshwork cells
JOURNAL	J. Biol. Chem. 273 (11), 6341-6350 (1998)
MEDLINE	98165818
REFERENCE	2 (bases 1 to 5300)
AUTHORS	Nguyen,T.D., Chen,P., Chen,H. and Polansky,J.R.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUN-1997) Ophthalmology, University of California San Francisco, 10 Kirkham Street, San Francisco, CA 94143-0730, USA
FEATURES	Location/Qualifiers
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promoter	/db_xref="taxon:9606"
mrna	1..>5300
	/gene="TIGR"
	1..5271
	/gene="TIGR"
	5272..>5300
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Db	421	TAATTAAGTATTTTGTTCTTGGGAAGAACCTCCATGTGACCTTGATGGGAAATATGGAA	480
Oy	481	aaagctcaaaagcatgatctgatcagatccccaagtgtgatbattattttaaaccagat	540
Db	481	AAAGCTCAAAAGCATGATCTGATGATCCCAAGTGGATTATTATTTAAAAACCGAT	540
Oy	541	ggcatcaactctgggggaagcaagttcagaaggtcaatgtttgcaaggaaacttaaacaaac	600
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Db	721	ATTGACTGGGCTAAAGCCCTGACATTTCAAAGGAATATGAAACATGAGACGCAAAACAAA	780
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Db	781	GACATGTTTAAAGGCAACGAAACATGTGAGCTTCAAGAGCAGCAGTGCCTCTCAGCA	840
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RESULT 2
HS4546/c 79376 bp DNA PRI 23-NOV-1999
LOCUS Human DNA sequence from PAC 4546 on chromosome 1q24. Contains
DEFINITION intracellular meshwork inducible glucocorticoid response protein,
TIGR, myocillin, ESTs and STS.
ACCESSION 298750.1 GI:2887277
VERSION 1q24: myocillin: TIGR.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 79376)
REFERENCE Direct Submission
AUTHORS Submitted (27-OCT-1997) Chromosome 1 Project Group
TITLE (http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton,
JOURNAL Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Feb 14, 1998 this sequence version replaced gi:2465060.
IMPORTANT: This sequence is not the entire insert of clone 4546.
It may be shorter because we only sequence overlapping sections
once, or longer because we arrange for a small overlap between
neighbouring submissions.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variations annotated may not be found in the sequence submission
corresponding to the overlapping clone as we submit sequences with
only a small overlap as described above.
This sequence was generated from part of bacterial clone contigs of
human chromosome 1, constructed by the Sanger Centre chromosome 1
mapping group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1/
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu) where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The true left end of clone 4546 is at 1 in this sequence. The true
left end of clone 56089 is at 79273.
4546 is from the library RPC13 constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong.
For further details see http://bacpac.med.buffalo.edu/
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incomplete repeat"
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DB 68346 TCCCTATTAACCTGTATAGCCTTCATTCGATGATGCTTTGGCAGGATGATTAAGATCA 68287					
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TITLE
JOURNAL
COMMENT

Howland-Pierre, N., Grant, G., Hagos, B., Heatford, A., Horton, L.,
Klein, J.C., Illey, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Lieu, C., Liu, G., Locke, K., Macdonald, P., Margulis, N., McCarthy, M.,
McEwen, P., McGuirk, A., McKernan, K., McPheeters, R., Melgrim, J.,
Meneus, L., Mihova, T., Miranda, C., Mlenaga, V., Morrow, J., Naylor, J.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Olivart, T.M.,
Peterson, K., Pierre, N., Pisanil, C., Pollara, V., Raymond, C.,
Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Tirrell, A.,
Travers, M., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B.,
Wu, X., Wyman, D., Ye, W.-J., Young, G., Zainoun, J., Zimmer, A. and
Zody, M.

Direct Submission
Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 25, 2000 this sequence version replaced g1:7249345.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RX/RepeatMasker.html>

Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
Center code: MIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L7153
Center clone name: 138_F_3

----- Summary Statistics -----
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator; Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 151483 bases at least Q40
Consensus quality: 160438 bases at least Q30
Consensus quality: 164708 bases at least Q20
Insert size: 167000; agarose-fp
Insert size: 167725; sum-of-ctrls
Quality coverage: 4.1 in Q20 bases; agarose-fp
Quality coverage: 4.1 in Q20 bases; sum-of-ctrls

* NOTE: This is a 'working draft' sequence. It currently
* consists of 28 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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1301 1400: gap of 100 bp
1401 2412: contig of 1012 bp in length
2413 2512: gap of 100 bp
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	*	29959	36225:	contig of 6567 bp	in length
	*	36226	36325:	gap of 100 bp	
	*	36326	44015:	contig of 7690 bp	in length
	*	44016	44115:	gap of 100 bp	
	*	44116	44943:	contig of 5378 bp	in length
	*	44949	44593:	gap of 100 bp	
	*	44594	56796:	contig of 7203 bp	in length
	*	56797	56896:	gap of 100 bp	
	*	56897	62860:	contig of 5564 bp	in length
	*	62861	62960:	gap of 100 bp	
	*	62961	72552:	contig of 9592 bp	in length
	*	72553	72652:	gap of 100 bp	
	*	72653	83310:	contig of 10658 bp	in length
	*	83311	83410:	gap of 100 bp	
	*	83411	92992:	contig of 9582 bp	in length
	*	92993	93092:	gap of 100 bp	
	*	93093	103886:	contig of 10794 bp	in length
	*	103887	103986:	gap of 100 bp	
	*	103987	119418:	contig of 14332 bp	in length
	*	119419	119518:	gap of 100 bp	
	*	119519	136695:	contig of 17177 bp	in length
	*	136696	136795:	gap of 100 bp	
	*	136796	153977:	contig of 17182 bp	in length
	*	153978	154077:	gap of 100 bp	
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Db 68782 AAATCTCAAAACAGACTTCCGGAAGTTATTCTTAAGAAATCTGTGTGTGTGTGTGTGTGT 68841
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Db 68842 AACCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 68901
Oy 5215 gggctgtcccccatatataaaactctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5271
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DEFINITION Homo sapiens myocilin (GLC1A) gene, promoter and exon 1.
ACCESSION AF049791
VERSION AF049791.1 GI:3065670
KEYWORDS
SEGMENT 1 of 3
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2800)
AUTHORS Fingert,J.H., Ying,L., Swiderski,R.E., Nystuen,A.M., Arbour,N.C.,
Alward,W.L.M., Sheffield,V.C. and Stone,E.M.
TITLE Characterization and comparison of the human and mouse GLC1A
glaucoma genes
JOURNAL Genome Res. (1998) In press
REFERENCE 2 (bases 1 to 2800)
AUTHORS Fingert,J.H., Ying,L., Swiderski,R.E., Nystuen,A.M., Arbour,N.C.,
Alward,W.L.M., Sheffield,V.C. and Stone,E.M.
TITLE Direct Submission
JOURNAL Submitted (23-FEB-1998) Ophthalmology, University of Iowa, 200
Hawkins Drive, Iowa City, IA 52242, USA
FEATURES
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Db 1 AGCCGACAGGAGGAGGAG-AAAAGAGAGGAGTATGATAGCAAGAAACAGATTGAT 59
Oy 3491 tcaaggcagtggaatattgcccacagggatattatgctcagtgatcctgtgtcttagag 3550
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Oy	3731	gcacaagggcgaatcccgctttcttcttcaacgggaagaaacatctccctaagtgtaagccaa	3790
Db	300	GCACAAGGGCATATCCCTTTCTTTTAAACAGAGAAATAATCTCTAAGGTAAACCCAA	359
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Oy	3851	atgcttactatctgtatctcaagaaatagagactgtaccccttggctcagctgttaacaaa	3910
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Oy	4570	aaaacaatcttctgaagaagaagttccccaagattccaccaatgaagttcttgcgaatgcaac	4629
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Dd	1139	ACACGAGATAGAACTGTATTAGAGGCTAACATTGCATTGGTGGCTTGAGATGCAAGACT	1258
Oy	4690	gaaatiaagaagcttcccccacaagaatacacacagtgttttaaaagctaagggttgaaagggaaa	4749
Dd	1259	GAAATTAGAAAGTTCTCCCAAGATACACAGTGTGTTTTAAGCTAGGCGGTGAAGGGGANA	1318
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Dd	1319	ATCTGCCCTTCCTTAGGAATGCTCTCCCGGAGCGCTGGTAAGGCTCCTGCTGTGTGTTT	1378
Oy	4810	tggcggctgttatcttccctctgccctgtctaaagcttaaagaacctgtgtgatctcca	4869
Dd	1379	TGGCTGGCTGTATTATTTTCTCTGTGCTCCCTGCTAGCTCTTAAGGACTTGTGTGANTCCA	1438
Oy	4870	gtccctaaagatgycctcgtgcacatgcaaggttcccatgactgttgcagaagtaatgana	4929
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Dd	1559	GTGTACGT	1618
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Dd	1619	TTATTTGGGGGTATGGGTGCATTAATTTGGATGTTCTTTTAAAAAGAAACTCCAAACAGAC	1678
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Dd	1679	TTCTGTGAAGCTTATTTTCTTAAGATCTTCTGTGGCAGCGCTGAAGGCAACCCCTGTGCAC	1738
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DEFINITION	Homo sapiens GLC1A (tribealicular meshwork response) gene, exon I, joined CDS.		Induced glucocorticoid
ACCESSION	J291171		
VERSION	291171.1	GI:2425156	
KEYWORDS	GLC1A.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
	1 (bases 1 to 1086)		
	Stone,E.M., Finger,T.H., Alward,W.L., Nguyen,T.D., Polansky,J.R.		
	Ritch,R., Kalenak,J.W., Craven,E.R. and Sheffield,V.C.		
	Identification of a gene that causes primary open angle glaucoma		
	Science 275 (5300), 668-670 (1997)		
TITLE	IDENTIFICATION OF A GENE THAT CAUSES PRIMARY OPEN ANGLE GLAUCOMA		
JOURNAL	SCIENCE		
MEDLINE	97158493		
REFERENCE	2 (bases 1 to 1086)		
AUTHORS	Adam,M.F., Belmondou,A., Binisti,P., Brezin,A.P., Valot,F.,		
	Beheboille,A., Descote,J.C., Copin,B., Gomez,L., Chaventre,A.,		
	Bach,J.F. and Garçon,H.J.		
	Recurrent mutations in a single exon encoding the evolutionarily		
	conserved olfactomedin-homology domain of TIGR in familial		
	open-angle glaucoma		
	Hum. Mol. Genet. 6 (12), 2091-2097 (1997)		
JOURNAL	HUM MOL GENET		
MEDLINE	97472461		
REFERENCE	3 (bases 1 to 1086)		

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Query Match          7.5%; Score 394.4; DB 9; Length 1228;
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OY 4922 gaatggaataataacagagaataatccttctgtaaatcagcacaccagtaagtcctg 4981
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DB 61 GAATGGAATAATAACAGAGAATAATATCCTTGTGAATATCAGCACACAGAGCCCTGCT 120

OY 4982 gtaagtgctgacgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 5041
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DB 121 GTAAGTGTGTGTAC--CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 178

OY 5042 aggaactatattgggtatgggtatgggtatgggtatgggtatgggtatgggtatgggtatgg 5101
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DB 179 AGGAACCTATTATTTGGGTATGGGTATGGGTATGGGTATGGGTATGGGTATGGGTATGGGTAT 238

OY 5102 aaacagactctggaaggtattcttcaagaatcttctgcaagcgtgaagcgaacccccc 5161
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OY 5162 ctatgcacagcccccacacacacacacacacacacacacacacacacacacacacacacac 5221
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DB 299 CTGTGCAACACCCGCCACCTCAGCTGCGACCTCTGTCTTCCGCCATGAAAGCGCTGG 358

OY 5222 ctcccccgtatataaactctctctgagcctcgagcctgagcagcagcagcagcagcagcag 5271
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RESULT 7
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LOCUS AC007688 Homo sapiens 12p12-27.2-31.7 BAC R111-392P7 (Roswell Park Cancer
DEFINITION Institute Human BAC Library) complete sequence.
ACCESSION AC007688
VERSION AC007688.15 GI:5815499
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 161577)
REFERENCE
AUTHORS Muzny,D., Arenson,A.D., Bouck,J., Bunac,C., Chen,Z., Ding,Y.,
Dugan,S., Durbin,J., Forcum,J., Garcia,C., Gorrell,J.H.,
Gottlieb,L.L., Hernandez,J., Issar,A., Jackson,L., Kneitz,S.,
Kondrjewski,N., Lau,S., Leal,B., Lee,E., Lichtenberg,O., Liu,W.,
Logan,O., Lu,J., Marondei,I., Martinez,C., Merscher,S., Miller,A.,
Montgomery,K., Oswal,G., Pampell,L.R., Parish,B.J., Perez,L.,
Rashid,N.D., Rives,C., Scherer,S.E., Shen,H., Shim,C., Simon,M.,
Vo,O., Williamson,A., Worley,K.C., Xiang,A.M., Yang,R., Yu,W.,
Zhou,X., Kucherlapati,R., Nelson,D. and Gibbs,R.A.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 161577)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (01-JUN-1999) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 161577)
REFERENCE 3
AUTHORS Morley,K.C.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
COMMENT On Sep 1, 1999 this sequence version replaced g1:5757565.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email

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gc-helpebcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features Listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Sult and P. Green, unpublished) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT-----

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----- Summary Statistics -----
Contig length: 161577
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Average error rate (BCM-Phrap estimate): 0.000163681
Fraction of Phrap values less than 40 : 0.0376047
Number of Consensus changing edits: 30
Number of N's in consensus : 0

----- Consensus changing edits -----
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47567 aaaaaaataa(n)ggaataaat aaaaaaataa(a)ggaataaat
51135 aaagaaagaa(n)aaagaaagaa aaagaaagaa(a)aaagaaagaa
75582 aaaaaaanaa(n)aaagaaagtt aaaaaaanaa(a)aaagaaagtt
75687 aaaaaaanaa(n)ggaatctcga ctaagaaagaa(a)aaagaaagtt
75687 aaaaaaanaa(n)aaagaaagtt aaaaaaanaa(a)aaagaaagtt
75752 tttaaaag(g)gcttgcctt tttaaaag(t)gcttgcctt
84017 gggagggaa(n)aaagaaagag gggagggaa(g)aaagaaagag
85227 ttgtttt(n)tgctttttt ttgtttt(c)tgctttttt
96681 ggaagtcag(n)atgcagttca aatctctaa(g)atgcagttca
111307 aatctctaa(n)ccgaaatcaa aatctctaa(g)ccgaaatcaa
11374 actaatatc(n)atccttttt actaatatc(t)atccttttt
11378 gtaacnaac(n)ttttttttt gtaacnaac(c)ttttttttt
112621 aaaaaaanaa(n)ccatctaga aaaaaaanaa(a)ccatctaga
135812 attcaacc(c)ttttttttt attcaacc(t)ttttttttt
137207 ttgcagcag(n)cgccacacag cgccacacag(c)cgccacacag
137218 cgccacacag(n)ctggcctaat gcaagtgaag(a)gattagaat
145113 gcaagtgaag(n)natgtaaat caagtgaag(g)atgtaaat
145114 caagtgaag(n)atgtaaat caagtgaag(g)atgtaaat
145232 ggcacggtg(n)ttcacacag ggcacggtg(c)ttcacacag
145233 ggcacggtg(n)ttcacacag ggcacggtg(c)ttcacacag
145238 ggtgctcac(n)ccagtaatcc ggtgctcac(g)ccagtaatcc
145321 gcaacatggt(c)nncccatc gcaacatggt(g)nncccatc

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145322 caacatggtc(n)ncccatct caacatggtc(a)aaccatctc
145323 aacatggtc(n)ncccatctc aacatggtc(a)aaccatctc
145324 aacatggtc(n)ncccatctc aacatggtc(a)aaccatctc
145363 gtccacacag(n)gtgtggtcgt gtccacacag(t)gtgtggtcgt
145377 gtgtggtcgtc(t)ctgtatctc gtgtggtcgtc(g)ctgtatctc
145397 taagtacttg(n)gaaggaagat taagtacttg(g)gaaggaagat
145505 aaaaaaaaa(n)gaaaaaaaaa aaaaaaaaa(a)gaaaaaaaaa

----- Distribution of Quality < 40 Bases -----

#	1000	900	800	700	600	500	400	300	200	100	0
bases	1000	900	800	700	600	500	400	300	200	100	0
Phrap Value Range	5	10	15	20	25	30	35	40			

Version: 1.01 gxf0.
Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="12p13.3"
/clone="RPC111-392p7"
complement(3..65)
repeat_region /rpt_family="MER4B"
161..471
complement(1607..702)
repeat_region /rpt_family="Alusx"
703..838
complement(839..916)
repeat_region /rpt_family="MIR"
complement(1205..1377)
repeat_region /rpt_family="MER104"
1388..1525
/standard_name="WIAF-759-STS"
/db_xref="dbSTS:65358"
1683..1971
repeat_region /rpt_family="AluJc"
1974..2261
repeat_region /rpt_family="AluJb"
2486..2593
repeat_region /rpt_family="MIR"
2610..3214
misc_feature /note="Region: unigene cluster similar to AA056332 and A1074576."
STS 2712..2823
/standard_name="SHGC-44583"
/db_xref="dbSTS:48451"
3185..3491
repeat_region /rpt_family="AluJb"
4509..5919
gene /gene="Human 5-hydroxytryptamine7 receptor isoform b mRNA, 068487."
repeat_region complement(6397..6537)
repeat_region /rpt_family="L2"
6967..7158
repeat_region /rpt_family="(CCCCG)n"
7094..7240
repeat_region /rpt_family="(CCG)n"

gene join(7241..7357,17979..18117,20062..20242,23659..23933)
/gene="unigene cluster containing N4239, R09325, and A1380369."
repeat_region complement(7770..8250)
/rpt_family="MER4B"
8831..9073
repeat_region /rpt_family="MER102"
complement(9075..9303)
repeat_region /rpt_family="L2"
9671..10135
repeat_region /rpt_family="LTR3A"
10426..10592
repeat_region /rpt_family="MIR"
10625..10689
repeat_region /rpt_family="MIR"
11094..11322
repeat_region /rpt_family="MIR"
complement(11985..12403)
/rpt_family="L2"

Query Match 3.6%; Score 189.8; DB 10; Length 161577;
Best Local Similarity 78.5%; Pred. No. 8e-31;
Matches 227; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 1280 aggtgaggtcgtgtcttaccctaccgtatgtcttaacacctgagctcactgaac 1339
DB 29160 AGAGTCTCAGCTATTACCGACGCTGAAGTGCAGTGGCGCAATCTGGCTATTGCAAC 29101
QY 1340 tctgctcccaaggtcgaacattctctgtctcagctcccggttaactggaataag 1399
DB 29100 TCTGCTCCCAAGTCAAGTGTCTCTGCTTACGCTTCCGAGTACTGGGACTACAG 29041
QY 1400 ggcgcgcgcgcgaattcttctgattgttagtaagatgaggtttcacacataagccg 1459
DB 29040 GCACACGCCACACTATTCTTCTATTATTAGACAGATGGGTTTGGCGATTGGCAG 28981
QY 1460 gctgtcttgaactctcgtacacctgaagtgatccaccctcagctccttaagtgctgg 1519
DB 28980 GCTGCTCTCAACCTCTGACCTGATCATCCACCCGCTCAGCTCTTAAGTGTGG 28921
QY 1520 attacagcatgagtcacgcgcgcgcgaaggtcagtggttaataag 1568
DB 28920 ATTACAGGtGtGAGCCACACGCCGCGCTGGAAGGgTTTAAGTAg 28872

RESULT 8
AC023790/c DNA HTG 25-JUL-2000
LOCUS Homo sapiens chromosome 12 clone RP11-377D9, WORKING DRAFT
DEFINITION SEQUENCE, 35 unordered pieces.
ACCESSION AC023790
VERSION AC023790.16 GI:9438256
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 19123)
AUTHORS Muzny D.M., Adams C., Bailey M., Barbara J., Blankenburg K.,
Bodota B., Bouck J., Bowie S., Brooks A., Buhay C., Bunec R.,
Burkett C., Burrows J., Carter M., Chacko J., Chen Z., Cox C.,
David R., Delgado D., Deshazo D., Ding Y., Donah-Rashid N.,
Dugan-Rocha S., Durbin K.J., Fernandez C., Ferraguto D.,
Forcum-Tansey J., Frantz P., Ganes R., Gorrell J.H., Gorrell L.L.,
Guevara W., Harris K., Hernandez J., Hodgson A., Hughes M.,
Holloway C., Hosak H., Jackson L.E., Jackson L., Jia Y., Jones M.,
Kelly S., Kondrjewski N., Kong Y., Kover C., Leal B., Li Z.,
Lichtarge O., Liu J., Liu W., Logan O., Lozano R.J., Lu J.,
Lucier R., Martin R., Martinez C., McLeod M.P., Mel G., Morgan M.,
Morriss S., Nash S., Nelson A., Nguyen R., Nguyen N., Nguyen S.,
Oswal G., Parish B., Paxton S., Payton B., Perez L., Pu L.L.,
Quiles M., Reiter D., Rives M., Samuel S., Say J., Scherer S.,
Shah E., Shen H., Simon M., Sparks A., Stamps A., Sucgang R.,

Tabor, P., Taylor, T., Vasquez, L., Vinson, R., Vo, Q., Wahbah, M.,
Watlington, S., Weinstein, G., Weinstein, I.R., Williamson, A.,
Worley, K., Wren, J., Wrensford, G., Yu, W., Zhou, X., Nelson, D. and
Gibbs, R.
Unpublished
Direct Submission
2 (bases 1 to 193123)
Worley, K.C.
Submitted (18-FEB-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 25, 2000 this sequence version replaced gi:9255941.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: HBM
Center clone name: RP11-377D9
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 167304 bases at least Q40
Consensus quality: 176244 bases at least Q30
Consensus quality: 181341 bases at least Q20
Estimated insert size: 180060; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-rip estimation
Quality coverage: 3.1x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 35 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
21094: contig of 21094 bp in length
21095
21194: gap of unknown length
21195
33930: contig of 12736 bp in length
33931
34030: gap of unknown length
34031
48318: contig of 14288 bp in length
48319
48418: gap of unknown length
48419
58799: contig of 10381 bp in length
58800
58899: gap of unknown length
58900
68723: contig of 9824 bp in length
68823
68824: gap of unknown length
68825
76073: contig of 7250 bp in length
76074
76173: gap of unknown length
76174
82868: contig of 6695 bp in length
82869
82968: gap of unknown length
82969
90046: contig of 7078 bp in length
90047
90146: gap of unknown length
90147
96141: contig of 5995 bp in length
96142
96241: gap of unknown length
96242
101873: contig of 5632 bp in length
101874
101973: gap of unknown length
101974
108002: contig of 6029 bp in length
108003
108102: gap of unknown length
108103
112903: contig of 4801 bp in length
112904
113003: gap of unknown length
113004
120209: contig of 7206 bp in length
120210
120309: gap of unknown length
120310
126353: contig of 6044 bp in length
126354
126453: gap of unknown length
126454
132888: contig of 6435 bp in length
132889
132988: gap of unknown length
132989
140137: contig of 7149 bp in length
140138
140237: gap of unknown length
140238
140239
144631: contig of 4394 bp in length

144632 144731: gap of unknown length
144732 150312: contig of 5581 bp in length
150313 150412: gap of unknown length
150413 150413: contig of 3702 bp in length
150414 154214: gap of unknown length
154215 154215: gap of unknown length
154216 158458: contig of 4244 bp in length
158459 158459: gap of unknown length
158460 161385: contig of 2827 bp in length
161386 161485: gap of unknown length
161486 164320: contig of 2835 bp in length
164321 164420: gap of unknown length
164421 167714: contig of 3294 bp in length
167715 176714: gap of unknown length
176715 171014: contig of 3200 bp in length
171015 171114: gap of unknown length
171115 173843: contig of 2729 bp in length
173844 173943: gap of unknown length
173944 176631: contig of 2688 bp in length
176632 176731: gap of unknown length
176732 178648: contig of 1917 bp in length
178649 178748: gap of unknown length
178749 180232: contig of 1484 bp in length
180233 180332: gap of unknown length
180333 183104: contig of 2772 bp in length
183105 183204: gap of unknown length
183205 184720: contig of 1516 bp in length
184721 184820: gap of unknown length
184821 186137: contig of 1317 bp in length
186138 186237: gap of unknown length
186238 188213: contig of 1976 bp in length
188214 188313: gap of unknown length
188314 190073: contig of 1760 bp in length
190074 190173: gap of unknown length
190174 191855: contig of 1682 bp in length
191856 191955: gap of unknown length
191956 193123: contig of 1168 bp in length.

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/db_xref="taxon:9606"
/chromosome="12"
/clone="RP11-377D9"

BASE COUNT 54294 a 41007 c 41291 g 53110 t 3421 others
ORIGIN
Query Match 3.6%; Score 189.8; DB 77; Length 193123;
Best Local Similarity 78.5%; Pred. No. 8e-31;
Matches 227; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
OY 1280 agggtaggggtctgtgtcttaccctacctaactctctacccctgaagctcactgaacc 1339
DB 134698 AAGTCTCACTCTATTACCACGCTGAAGTGCAGTGGCGCAATCTCGCTCTTCCACCC 134639
OY 1340 tctgtctcccaaggtccaagaactctctctgtctcagccctcccgctagctggactaag 1339
DB 134638 TCTGCTCTCCACAGTCAAGTATTTCTCTGCTTACGCTTCCGCACTACTGCGATACAG 134579
OY 1400 ggcacagcccgccgaattcttctgattctgtagagatgaggggtttaccataattgcccg 1459
DB 134578 GCACACGCCACCTAATTTTGTATTATTAGTACAGATGGGGTTTGGCGTATGGCCAG 134519
OY 1460 gctgtctcgaactctcgaactcgaagtgatccaccacactcagctctcttaagtgctggg 1519
DB 134518 GCTGTCTCAACTCTGCTGCTCAGGTATCCACCGCTCAGCTCTTAAGTCTGGG 134459
OY 1520 attcaagcatagtcacacgcccgcgcaagggcagtggttttaataag 1568
DB 134458 ATTACAGGTGTAGCCACACCGCCGCTGGAAGGGTTTAAAGTAC 134410
RESULT 9
AC012404

TITLE The sequence of Homo sapiens PAC clone RP5-113911
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 97037)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 97037)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (03-OCT-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE 5 (bases 1 to 97037)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (18-MAR-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE 6 (bases 1 to 97037)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Oct 3, 1998 this sequence version replaced g1:3213024.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: saplens@wustl.wustl.edu
----- Summary Statistics
Center project name: H_DJ1139101

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
This sequence was generated from part of bacterial clone contigs of
human chromosome X, constructed by the chromosome X mapping group
at the Sanger Centre, Wellcome Trust Genome Campus, Hinxton, UK.
Further information can be found at
http://www.sanger.ac.uk/HGP/ChrX/

SOURCE INFORMATION:
This clone was derived from human PAC library RPC1-5, prepared by
Pieter de Jong and coworkers at the Roswell Park Cancer Institute
(http://dscpac.med.buffalo.edu) using the method described by
Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from
one male donor.
The clone may be obtained either from Genome Systems, Inc.
(http://www.genomesystems.com) or Research Genetics, Inc.
(http://www.resgen.com); or from Pieter de Jong.
VECTOR: pCYPAC2
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP4-555N2; the clone sequenced
to the right is RP3-404F18, 200 bp overlap. Actual start of this
clone is at base position 1 of RP5-113911; actual end is at 13269
of RP3-404F18.

FEATURES
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1. 97037
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"

/map="Xq23"
/clone="RP5-113911"
/clone_1fb="RPC1-5"
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Repeat_region
830..1035
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Repeat_region
2179..2349
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Repeat_region
3434..3489
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Repeat_region
3526..3739
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4681..4852
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10974..11111
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Repeat_region
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12859..13433
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13435..13564
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repeat_region 19605..20227
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repeat_region 20848..21707
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repeat_region 21717..22111
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repeat_region 22866..23031
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repeat_region 24203..24554
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repeat_region 25106..25479
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Query Match 3.68; Score 187.8; DB 9; Length 97037;

Best Local Similarity 78.78; Pred. No. 2,1e-30; Matches 240; Conservative 0; Mismatches 57; Indels 8; Gaps 1;

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OY 1280 agggtagggctgctgctcaccctacgtctagctcctacactgagctgagctcaacc 1339
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DB 54922 AGAGTCTTGTCTCTCTCATCCAGTGCAGTGCAGTGCAGCATCTCAGCTTACAC 5463
OY 1340 tctgctccaggtctcaagaatctcctgctcagcctccgcgtagcttggactaac 1399
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DB 54862 TCTGCTCTCTGGGTTCAAGCATCTCTCTCAGCCTCCGAGTACGCTGGACTACAG 54803
OY 1400 gcg-----caegccgcgctaatttttctatctgtatgtagaatagggtttcacata 1451
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DB 54802 GCCGATGCCACACGCCACCTAATTTTGTATTTAGTAGAGATGGGTTTACCATTA 54743
OY 1452 ttgagccgctgctgctgactcctgagcctcaggtgataccaccactcagcctctaa 1511
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DB 54742 TTGCTCAGGCTGGCTTGAACCTCTGACCTGATGATCCCTGCTCGGCTCCCAAA 54683
OY 1512 gtctggtatatacagcatgataccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1571
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DB 54682 GTGCTGGGATTACAGGGGTGAGCCAGCGCGCGCTCTCTTCTGATTTTGGATGTA 54623
OY 1572 taact 1576
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DB 54622 CAAT 54618

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RESULT 11
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 LOCUS HUMW703 135038 bp DNA PRI 24-DEC-1996
 DEFINITION Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.
 ACCESSION L78810

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VERSION L78810.1 GI:1381111
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 135038)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
TITLE Chen,C.N., Su,Y., Baybayan,P., Siruno,A., Nagaraja,R.,
Mazzarella,R., Schlessinger,D. and Chen,E.
JOURNAL Ordered shotgun sequencing of a 135 kb Xq25 YAC containing ANT2 and
MEDLINE four possible genes, including three confirmed by EST matches
97078684 Nucleic Acids Res. 24 (20), 4034-4041 (1996)
COMMENT Submitted by:
Elison Chen.
Advanced Center for Genetic Technology,
Applied Biosystems Division of Perkin Elmer Corp., 850 Lincoln
Center Drive,
Foster City, CA 94404 USA
and
David Schlessinger,
Department of Molecular Microbiology and Center for Genetics in
Medicine
Washington University School of Medicine,
St. Louis MO 63110 USA
E-mail: elison@genseq.apd.bio.com and davis@genetics.wustl.edu
Note: Gene predictions were accomplished with runs of Grail
versions 1.1 and 1.2, coupled with fasta and blastx comparisons to
genbank & non-redundant peptide libraries. Repeat analysis was
accomplished via censor.
The Rat EST105369 shows significant homology via blastx to this
sequence
Strand Start End
top 9072 9326
The Graves Disease carrier protein (X66035) shows significant
homology via blastx to this sequence
Strand Start End
top 28802 29076
top 35858 36081
Comments for gene ANT-2 :
This gene shows homology via blastx to the EST clone y115a12 Strand
Start End
bottom 125256 125915.
location/Qualifiers
1..135038
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="X"
/complement(271..560)
/rpt_family="Alu-Sx"
/evidence=experimental
/complement(774..1726)
/rpt_family="L1"
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/complement(1842..2131)
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/rpt_family="MLTIC"
/evidence=experimental
3204..3325
/complement(3204..3325)
/rpt_family="MIR2"
/evidence=experimental
3384..35674
/rpt_family="Alu-Sg"
/evidence=experimental
3794..4216

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repeat_unit	/rpt_family="L1MA9" /evidence-experimental 7502. .7792 /rpt_family="Alu-J" /evidence-experimental 7965. 8072 /rpt_family="L1MA2" /evidence-experimental 8073. .8360 /rpt_family="Alu-Sx" /evidence-experimental 8379. 8535 /rpt_family="L1MA5" /evidence-experimental 8540. .8743 /rpt_family="L1" /evidence-experimental 8744. 8869 /rpt_family="Alu-J" /evidence-experimental complement(9771. .10055) /rpt_family="Alu-Sx" /evidence-experimental 10292. 10780 /rpt_family="L1" /evidence-experimental 11403. .11692 /rpt_family="Alu-Sx" /evidence-experimental 12097. 12459 /rpt_family="MST" /evidence-experimental complement(12492. .12701) /rpt_family="Alu-J or an Alu-S" /evidence-experimental complement(12730. .13020) /rpt_family="Alu-Sx" /evidence-experimental 13708. .13997 /rpt_family="Alu-Sg" /evidence-experimental complement(14402. .14541) /rpt_family="MIR2" /evidence-experimental 14546. .14836 /rpt_family="Alu-Sx" /evidence-experimental 15348. .15628 /rpt_family="Alu-Sx" /evidence-experimental complement(15805. .16906) /rpt_family="LRR12" /evidence-experimental 17388. .17930 /rpt_family="MERA4" /evidence-experimental complement(20000. .20276) /rpt_family="Alu-Sb0 or an Alu-Sb1" /evidence-experimental 20353. .20856 /rpt_family="L1ME3A" /evidence-experimental 20900. .20986 /rpt_family="MSTA" /evidence-experimental 20988. .21276 /rpt_family="Alu-Sx" /evidence-experimental 21342. .21723 /rpt_family="L1ME3A" /evidence-experimental 21841. .22129 /rpt_family="Alu-Sp"
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Query Match	Best Local Similarity	Matches 240: Conservative	Score 187.8: DB 67: Length 135038:
1280	agggtgagggctgtgtcttacacctacacctgtatgctctacacctgagctacgtgaacc	1339	
8349	AGAGCTTGCTGCTGTCATCCAAAGCTGGAGTGGCAAGTGGCAGATCTGACTGCAACC	8290	
1340	tctgctcccaaggttcaagaattctcctgtctcagccctccgctgtagctgggaactcaag	1399	
8289	TCTGCTCTCTGGGTTCAGAGCAATCTCTCTGCTCAGCCTCCGAGTGGCTGGACTACAG	8230	
1400	ggg-----cagcccggttaatttttgatgttaagttagagatgagggtttcacacata	1451	
8229	GGCGATGCCACACAGCCCGAGCTAATTTTGTATTTAGTAGAGATGGGTTTCACCAATA	8170	
1452	taagcccgctgtgtcttgaactctctgaacctcaagtgatccaccacactcagcctctctaa	1511	
8169	TTGGTGACAGGCTGGTCTTGAATCTCTGACGTCAAGTATGATCCACAGCTGGCTGGCTCCCAA	8110	
1512	gtgtgtggtattacaggatgagtcaccgctggccgagccaaggttcaagtgtttaaagaa	1571	

|||||
Db 8109 GTGCTGGATTACAGCGGTAGACCGCGCGCGCTCTTCTAGTATTTGCAATGTA 8050
Oy 1572 taact 1576
Db 8049 CAAT 8045
RESULT 12
LOCUS HS821D11/c
DEFINITION Human DNA sequence from clone RP5-821D11 on chromosome 22q12.3-13.1
Accession AL021453.1 GI:3413288
Version AL021453.1
Keywords HTG: D22S1157; SREBF2; Sterol Regulatory Element Binding
Source Transcription Factor 2.
Organism human.
Reference Homo sapiens
Authors Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Journal 1 (bases 1 to 76727)
Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
Requests: clonerequest@sanger.ac.uk
On Aug 12, 1998 this sequence version replaced g1:3355590.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
This sequence was generated from part of bacterial clone contigs of
human chromosome 22, constructed by the Sanger Centre Chromosome 22
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr22
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/Celegans/wormpep RP5-821D11 is
from the library RPCI-5 constructed at the Roswell Park Cancer
Institute by the group of Pieter de Jong. For further details see
http://daccpac.med.buffalo.edu/
VECTOR: pCYPAC2
IMPORTANT: This sequence is not the entire insert of clone
RP5-821D11. It may be shorter because we only sequence overlapping
sections once, or longer because we arrange for a small overlap
between neighbouring submissions.
The true left end of clone RP5-821D11 is at 1 in this sequence. The
true right end of clone CTA-10966 is at 42082 in this sequence. The
start of this sequence overlaps with sequence 297716 The end of
this sequence overlaps with sequence 283840.
Location/Qualifiers
1..76727
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="22"
/map="q12.3-13.1"
/clone="RP5-821D11"

repeat_region /clone_lib="RPCI-5"
350..434
/note="12 repeat: matches 2490. .2537 of consensus"
repeat_region 435..743
/note="AluJb repeat: matches 8. .312 of consensus"
variation 446..448
/note="clone CTA-10966
tct in this entry
substitution"
/replace="ttt"
744..840
/note="12 repeat: matches 2381. .2490 of consensus"
join(1230..1711,13695..13736)
/gene="dJ821D11.1"
/note="match: ESTs: Em:AA419437"
/evidence="not experimental"
/product="dJ821D11.1 (PUTATIVE protein)"
1230..13736
/gene="dJ821D11.1"
1314..1316
/gene="dJ821D11.1"
/note="clone CTA-10966
tgt in this entry
substitution"
/replace="tct"
join(1601..1711,13695..13736)
/gene="dJ821D11.1"
/note="other possible startcodon at 1583
this gene and dJ821D11.2 could be part of one gene
match: proteins: Tr:095505"
/codon_start=1
/evidence="not experimental"
/product="dJ821D11.1 (PUTATIVE protein)"
/protein_id="CAA16279.1"
/db_xref="GI:4200330"
/db_xref="SPTRFEMBL:095505"
/translation="MLALTAKADSPRTALCSAWLTPAFSAQOHKGSLOKDPLLSO
ACVGCLE"
1760..1762
/gene="dJ821D11.1"
/note="clone CTA-10966
gag in this entry
substitution"
/replace="ggg"
1773..1923
/note="MIR repeat: matches 47. .201 of consensus"
1901..1903
/gene="dJ821D11.1"
/note="clone CTA-10966
tca in this entry
substitution"
/replace="tta"
2010..2209
/note="12 repeat: matches 2250. .2453 of consensus"
2302..2304
/gene="dJ821D11.1"
/note="clone CTA-10966
gga in this entry
substitution"
/replace="gaa"
3042..3152
/note="LMC1 repeat: matches 6231. .6332 of consensus"
3162..3457
/note="AluSp repeat: matches 1. .297 of consensus"
3458..3551
/note="MIR repeat: matches 74. .148 of consensus"
3552..3848
/note="AluJb repeat: matches 1. .299 of consensus"
3849..3887
/note="MIR repeat: matches 32. .74 of consensus"
4753..4754
/gene="dJ821D11.1"
/note="clone CTA-10966

[illegible]

Qy	1340	tcgcgtcccaaggttcaagcaatttcctctgtctcaagcccccgttaactggagatacag	1399
Db	57358	tctgccttcccaaggttcaagtaatttctctgtctctgcctctcgcctctcggggttctgggactatnag	572939
Qy	1400	gcgc-----cagcccgactaattttgtatgtgttagtaagaatggaggtttcacacata	1451
Db	57298	gcggttacccaccatcccgccgaattttttgtatttttagtaagatggcggtttcacacata	57239
Qy	1452	ttagcccgagctgtctttaaacctccggaactcagatgataccacacactcagcctctata	1511
Db	57238	ttggcttagcctgtgtttgaactcttgacctcagatgataccgcccaacttcggcctcccaaa	57179
Qy	1512	gtgcctggagattcaagacatgagtcacccgcgcgcgcacaaaggttcagtgttataaagaa	1571
Db	57178	gtgcctggagattcaagacatgagtcacccgcgcgcgcacaaatctgggtattttcaaatgaa	57119
Qy	1572	taa 1574	
Db	57118	aaa 57116	

RESULT	13
LOCUS	AC026395/c
DEFINITION	AC026395 152044 bp DNA HTG 15-JUN-2000
ACCESSION	Homo sapiens chromosome 10 clone RP11-45D20, WORKING DRAFT
VERSION	AC026395.3 GI:8567738
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 152044) Smith,D.R. Genome Therapeutics Corporation Sequencing Center; Human Genome Sequence Data Unpublished 2 (bases 1 to 152044) Smith,D.R. Direct Submission Submitted (22-MAR-2000) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA On Jun 15, 2000 this sequence version replaced gi:7330305.
JOURNAL	
TITLE	
AUTHORS	
COMMENT	

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Quality coverage: 3.2x in Q20 bases; sum-of-coverage:
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 44 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
*
*      1      1006: contig of 1006 bp in length
*      1007      1106: gap of unknown length
*      1107      2475: contig of 1369 bp in length
*      1107      2575: gap of unknown length
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* 2576 3927: contig of 1352 bp in length
* 3928 4027: gap of unknown length
* 4028 5333: contig of 1306 bp in length
* 5334 5433: gap of unknown length
* 5434 6564: contig of 1131 bp in length
* 6565 6664: gap of unknown length
* 6665 7870: contig of 1206 bp in length
* 7871 9384: contig of 1414 bp in length
* 9385 9484: gap of unknown length
* 9485 10791: contig of 1307 bp in length
* 10792 10891: gap of unknown length
* 10892 13010: contig of 2119 bp in length
* 13011 13110: gap of unknown length
* 13111 14617: contig of 1507 bp in length
* 14618 14717: gap of unknown length
* 14718 16217: contig of 1500 bp in length
* 16218 16317: gap of unknown length
* 16318 18106: contig of 1789 bp in length
* 18107 18206: gap of unknown length
* 18207 19498: contig of 1292 bp in length
* 19499 19598: gap of unknown length
* 19599 20867: contig of 1269 bp in length
* 20868 20967: gap of unknown length
* 20968 22203: contig of 1236 bp in length
* 22204 24098: contig of 1795 bp in length
* 24099 24198: gap of unknown length
* 24199 26005: contig of 1807 bp in length
* 26006 26105: gap of unknown length
* 26106 27441: contig of 1336 bp in length
* 27442 29037: contig of 1496 bp in length
* 29038 29138: gap of unknown length
* 29139 30660: contig of 1523 bp in length
* 30661 30760: gap of unknown length
* 30761 32755: contig of 1995 bp in length
* 32756 32855: gap of unknown length
* 32856 34483: contig of 1628 bp in length
* 34484 34583: gap of unknown length
* 34584 37578: contig of 2895 bp in length
* 37579 37678: gap of unknown length
* 37679 39699: contig of 2021 bp in length
* 39700 39799: gap of unknown length
* 39800 42411: contig of 2612 bp in length
* 42412 42511: gap of unknown length
* 42512 45638: contig of 3127 bp in length
* 45639 45738: gap of unknown length
* 45739 49739: contig of 4001 bp in length
* 49740 49839: gap of unknown length
* 49840 54276: contig of 4437 bp in length
* 54277 54376: gap of unknown length
* 54377 59051: contig of 4675 bp in length
* 59052 59151: gap of unknown length
* 59152 64626: contig of 5475 bp in length
* 64627 67988: contig of 3262 bp in length
* 67989 68088: gap of unknown length
* 68089 72494: contig of 4406 bp in length
* 72495 72594: gap of unknown length
* 72595 75643: contig of 3049 bp in length
* 75644 75743: gap of unknown length
* 75744 79510: contig of 3767 bp in length
* 79511 79610: gap of unknown length
* 79611 84664: contig of 5054 bp in length
* 84665 84764: gap of unknown length
* 84765 90514: contig of 5750 bp in length
* 90515 90614: gap of unknown length
* 90615 96185: contig of 5571 bp in length
* 96186 96285: gap of unknown length
* 96286 102048: contig of 5763 bp in length
* 102049 102148: gap of unknown length
* 102149 108361: contig of 6213 bp in length

* 108362 108461: gap of unknown length
* 108462 114329: contig of 5868 bp in length
* 114330 114429: gap of unknown length
* 114430 120644: contig of 6315 bp in length
* 120645 120744: gap of unknown length
* 120745 128025: contig of 7281 bp in length
* 128026 128125: gap of unknown length
* 128126 138788: contig of 10663 bp in length
* 138789 138888: gap of unknown length
* 138889 152044: contig of 13156 bp in length.
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/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-45D20"
/clone_11b="RPC1-11"
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Best Local Similarity 80.8%: Pred. No. 5.7e-30; Indels 8; Gaps 1;
Matches 232; Conservative 0; Mismatches 47;

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Db 30398 ATCTGGCTCACTGCACTCCACCTCCGGGTTCAATGATTCCTCCGCTCAGCCTCC 30339
Oy 1381 cgcgtagctgggaactaagc-----gaagcccggaattttgttgtta 1432
Db 30338 TGAGTAGCTGGGATTAACAGCACCCACTACACCGCCAGTAAATTTTGTATTTTACTA 30279
Oy 1433 gagatggggtttaccatattagccggctgtcttgaacctccagctcaggtatca 1492
Db 30278 GAGATGGGGTTTACCATGTTGGCCAGCTGTCTTGAACCTCTGACTCAGGTATCCA 30219
Oy 1493 cccacctgaacctcctaaagcttggaattacaggaatgaatcagcgccgcccagag 1552
Db 30218 CCGGCTTAGCCTCCCAAGTGCTGGATTAACGATGACGACGACCTGCGCCCAATT 30159
Oy 1553 gtcaagtgttaataagaataactgaatgttacttaaccaacag 1599
Db 30158 TTAATTTTTTTAAAGAAAATGTGATATTTAAAAAACACAG 30112
RESULT 14
LOCUS AC025947 157057 bp DNA HTG 10-JUN-2000
DEFINITION Homo sapiens chromosome 10 clone RP11-78A18, WORKING
DRAFT SEQUENCE, 26 unordered pieces.
ACCESSION AC025947
VERSION AC025947.3 GI:8439851
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 157057)
AUTHORS Smith,D.R.
TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome
Sequence Data
JOURNAL Unpublished
AUTHORS Smith,D.R.
TITLE Direct Submission
REFERENCE Submitted (18-MAR-2000) Genome Therapeutics Corporation, 100 Beaver
JOURNAL Street, Waltham, MA 02453, USA
COMMENT On Jun 10, 2000 this sequence version replaced gi:7528340.

Center: Genome Therapeutics Corporation
Center code: GTC
Web site: http://www.genomecorp.com/


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----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIRB
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L3895
Center clone name: 20_F_6
----- Summary Statistics
Sequencing vector: M13: M77815: 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 152793 bases at least Q40
Consensus quality: 156653 bases at least Q30
Consensus quality: 158136 bases at least Q20
Insert size: 160000: agarose-fp
Insert size: 159999: sum-of-contigs
Quality coverage: 5.9 in Q20 bases; agarose-fp
Quality coverage: 5.9 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
2207 2306: gap of 100 bp in length
2307 2306: gap of 100 bp in length
2307 6910: contig of 4604 bp in length
6911 7010: gap of 100 bp
7011 9818: contig of 2808 bp in length
9819 9918: gap of 100 bp
9919 13394: contig of 3476 bp in length
13395 13494: gap of 100 bp
13495 17122: contig of 3628 bp in length
17123 17222: gap of 100 bp
17223 19752: contig of 2530 bp in length
19753 19852: gap of 100 bp
19853 23958: contig of 4106 bp in length
23959 24058: gap of 100 bp
24059 29684: contig of 5626 bp in length
29685 29784: gap of 100 bp
29785 33951: contig of 4167 bp in length
33952 34051: gap of 100 bp
34052 39841: contig of 5790 bp in length
39842 39941: gap of 100 bp
39942 48297: contig of 8356 bp in length
48298 48397: gap of 100 bp
48398 56898: contig of 8501 bp in length
56899 56998: gap of 100 bp
56999 65924: contig of 8926 bp in length
65925 66024: gap of 100 bp
66025 81114: contig of 15090 bp in length
81115 81214: gap of 100 bp
81215 112500: contig of 31286 bp in length
112501 112600: gap of 100 bp
112601 161499: contig of 48899 bp in length.
Location/Qualifiers
1. 161499
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/db_xref="taxon:9606"
/clone_1bp="RP11-20F6"
/clone_1bp="RP11 Human Male BAC"
1. 2206
/note="assembly_fragment"
2307. .6910
/note="assembly_fragment"
7011. .9818
/note="assembly_fragment"
9919. .13394
/note="assembly_fragment"
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/note="assembly_fragment"
misc_feature 17223..19752
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vector_side:right"
misc_feature 19853..23958
/note="assembly_fragment"
misc_feature 24059..29684
/note="assembly_fragment"
misc_feature 29785..33951
/note="assembly_fragment"
misc_feature 34052..39841
/note="assembly_fragment"
misc_feature 39942..48297
/note="assembly_fragment"
misc_feature 48398..56898
/note="assembly_fragment"
misc_feature 56999..65924
/note="assembly_fragment"
misc_feature 66025..81114
/note="assembly_fragment"
clone_end:SP6
vector_side:left"
misc_feature 81215..112500
/note="assembly_fragment"
misc_feature 112601..161499
/note="assembly_fragment"
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BASE COUNT 44611 a 37543 c 36473 g 41370 t 1502 others
ORIGIN
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Query Match 3.5%; Score 185.8; DB 72; Length 161499;
Best Local Similarity 77.1%; Pred. No. 5.8e-30;
Matches 226; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
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OY 1283 gtgaggctcgtgtcttaacacctcctgtatgctctacacctgagctcaactgacctc 1342
|| || || || || || || || || || || || || || || || || || || || || ||
Db 16769 GTCTTGCTCTGTCAACGAGCTGGAGGCGAGTGACACCATCTCGCTCACTGCAACTCT 16828

OY 1343 gccctccaggttcaggaattcctcgtctcagacctccgcgtagctggagctacagagc 1402
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 16829 GCGTCCAGATTCAAGCAATTTCTCTCAGCTCTAGCTCTAGTACTGGGGTTATAGCA 16888

OY 1403 cagcccgctaatcttctgattgtagtagagatgggtttcacatattagcccgct 1462
|| || || || || || || || || || || || || || || || || || || || || ||
Db 16889 CATGCCAGGCAATTTTGTGTTTGTAGTAGAGATGGGTTTGCCATGTTGCCAGGCT 16948

OY 1463 ggtctgaactcctgacctgaagtgtatcacaccacctcagctcctcctaagtgtcggaat 1522
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 16949 GGTCTGAACCTCCAGACTCAGATGATCCCGCCGCTGCCCAAGTGTGGGATT 17008

OY 1523 acaagcatgagtcacggccgcgcgaagggttcagtggttaataagaagtaaac 1575
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 17009 ACAGGTGTGAGCCACCGCGCCACGACCTATTTTTAATTTTATTTTATCAAC 17061
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Search completed: December 3, 2000, 19:17:56
Job time: 46490 sec
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